Full wwPDB X-ray Structure Validation Report (i)

Feb 18, 2024 – 11:00 AM EST

PDB ID	:	4ECE
Title	:	Crystal structure of purine nucleoside phosphorylase (W16Y, W94Y, W178Y, H257W) mutant from human complexed with guanine
Authors	:	Haapalainen, A.M.; Ho, M.C.; Suarez, J.J.; Almo, S.C.; Schramm, V.L.
Deposited on	:	2012-03-26
Resolution	:	2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

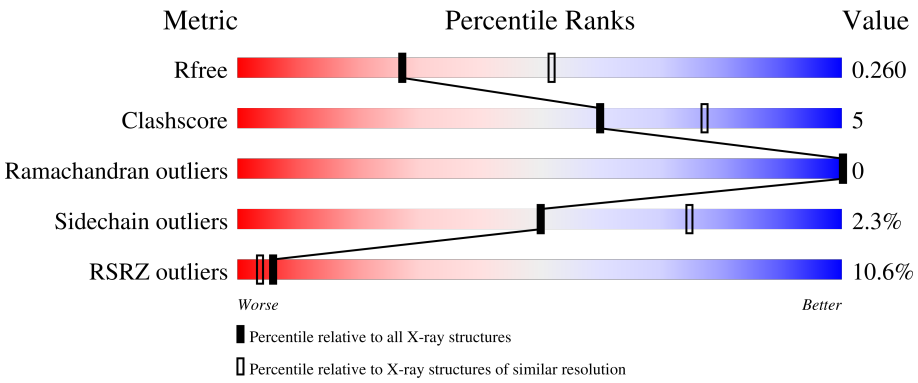
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	324	3% 75% 12% • 13%
1	B	324	2% 76% 11% 13%
1	C	324	4% 75% 12% 13%
1	D	324	5% 77% 10% 13%
1	E	324	11% 78% 9% • 13%

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Mol	Chain	Length	Quality of chain
1	F	324	30% 77% 10% 13%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 13632 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Purine nucleoside phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	282	2206	1405	382	403	16	0	1	0
1	B	283	2216	1411	383	406	16	0	1	0
1	C	283	2219	1413	383	406	17	0	2	0
1	D	282	2214	1410	385	403	16	0	2	0
1	E	282	2203	1403	382	403	15	0	0	0
1	F	282	2203	1403	382	403	15	0	0	0

There are 240 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-34	MET	-	initiating methionine	UNP P00491
A	-33	ARG	-	expression tag	UNP P00491
A	-32	GLY	-	expression tag	UNP P00491
A	-31	SER	-	expression tag	UNP P00491
A	-30	HIS	-	expression tag	UNP P00491
A	-29	HIS	-	expression tag	UNP P00491
A	-28	HIS	-	expression tag	UNP P00491
A	-27	HIS	-	expression tag	UNP P00491
A	-26	HIS	-	expression tag	UNP P00491
A	-25	HIS	-	expression tag	UNP P00491
A	-24	GLY	-	expression tag	UNP P00491
A	-23	MET	-	expression tag	UNP P00491
A	-22	ALA	-	expression tag	UNP P00491
A	-21	SER	-	expression tag	UNP P00491
A	-20	MET	-	expression tag	UNP P00491
A	-19	THR	-	expression tag	UNP P00491
A	-18	GLY	-	expression tag	UNP P00491

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	GLY	-	expression tag	UNP P00491
A	-16	GLN	-	expression tag	UNP P00491
A	-15	GLN	-	expression tag	UNP P00491
A	-14	MET	-	expression tag	UNP P00491
A	-13	GLY	-	expression tag	UNP P00491
A	-12	ARG	-	expression tag	UNP P00491
A	-11	ASP	-	expression tag	UNP P00491
A	-10	LEU	-	expression tag	UNP P00491
A	-9	TYR	-	expression tag	UNP P00491
A	-8	ASP	-	expression tag	UNP P00491
A	-7	ASP	-	expression tag	UNP P00491
A	-6	ASP	-	expression tag	UNP P00491
A	-5	ASP	-	expression tag	UNP P00491
A	-4	LYS	-	expression tag	UNP P00491
A	-3	ASP	-	expression tag	UNP P00491
A	-2	PRO	-	expression tag	UNP P00491
A	-1	THR	-	expression tag	UNP P00491
A	0	LEU	-	expression tag	UNP P00491
A	16	TYR	TRP	engineered mutation	UNP P00491
A	51	SER	GLY	engineered mutation	UNP P00491
A	94	TYR	TRP	engineered mutation	UNP P00491
A	178	TYR	TRP	engineered mutation	UNP P00491
A	257	TRP	HIS	engineered mutation	UNP P00491
B	-34	MET	-	initiating methionine	UNP P00491
B	-33	ARG	-	expression tag	UNP P00491
B	-32	GLY	-	expression tag	UNP P00491
B	-31	SER	-	expression tag	UNP P00491
B	-30	HIS	-	expression tag	UNP P00491
B	-29	HIS	-	expression tag	UNP P00491
B	-28	HIS	-	expression tag	UNP P00491
B	-27	HIS	-	expression tag	UNP P00491
B	-26	HIS	-	expression tag	UNP P00491
B	-25	HIS	-	expression tag	UNP P00491
B	-24	GLY	-	expression tag	UNP P00491
B	-23	MET	-	expression tag	UNP P00491
B	-22	ALA	-	expression tag	UNP P00491
B	-21	SER	-	expression tag	UNP P00491
B	-20	MET	-	expression tag	UNP P00491
B	-19	THR	-	expression tag	UNP P00491
B	-18	GLY	-	expression tag	UNP P00491
B	-17	GLY	-	expression tag	UNP P00491
B	-16	GLN	-	expression tag	UNP P00491

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	GLN	-	expression tag	UNP P00491
B	-14	MET	-	expression tag	UNP P00491
B	-13	GLY	-	expression tag	UNP P00491
B	-12	ARG	-	expression tag	UNP P00491
B	-11	ASP	-	expression tag	UNP P00491
B	-10	LEU	-	expression tag	UNP P00491
B	-9	TYR	-	expression tag	UNP P00491
B	-8	ASP	-	expression tag	UNP P00491
B	-7	ASP	-	expression tag	UNP P00491
B	-6	ASP	-	expression tag	UNP P00491
B	-5	ASP	-	expression tag	UNP P00491
B	-4	LYS	-	expression tag	UNP P00491
B	-3	ASP	-	expression tag	UNP P00491
B	-2	PRO	-	expression tag	UNP P00491
B	-1	THR	-	expression tag	UNP P00491
B	0	LEU	-	expression tag	UNP P00491
B	16	TYR	TRP	engineered mutation	UNP P00491
B	51	SER	GLY	engineered mutation	UNP P00491
B	94	TYR	TRP	engineered mutation	UNP P00491
B	178	TYR	TRP	engineered mutation	UNP P00491
B	257	TRP	HIS	engineered mutation	UNP P00491
C	-34	MET	-	initiating methionine	UNP P00491
C	-33	ARG	-	expression tag	UNP P00491
C	-32	GLY	-	expression tag	UNP P00491
C	-31	SER	-	expression tag	UNP P00491
C	-30	HIS	-	expression tag	UNP P00491
C	-29	HIS	-	expression tag	UNP P00491
C	-28	HIS	-	expression tag	UNP P00491
C	-27	HIS	-	expression tag	UNP P00491
C	-26	HIS	-	expression tag	UNP P00491
C	-25	HIS	-	expression tag	UNP P00491
C	-24	GLY	-	expression tag	UNP P00491
C	-23	MET	-	expression tag	UNP P00491
C	-22	ALA	-	expression tag	UNP P00491
C	-21	SER	-	expression tag	UNP P00491
C	-20	MET	-	expression tag	UNP P00491
C	-19	THR	-	expression tag	UNP P00491
C	-18	GLY	-	expression tag	UNP P00491
C	-17	GLY	-	expression tag	UNP P00491
C	-16	GLN	-	expression tag	UNP P00491
C	-15	GLN	-	expression tag	UNP P00491
C	-14	MET	-	expression tag	UNP P00491

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-13	GLY	-	expression tag	UNP P00491
C	-12	ARG	-	expression tag	UNP P00491
C	-11	ASP	-	expression tag	UNP P00491
C	-10	LEU	-	expression tag	UNP P00491
C	-9	TYR	-	expression tag	UNP P00491
C	-8	ASP	-	expression tag	UNP P00491
C	-7	ASP	-	expression tag	UNP P00491
C	-6	ASP	-	expression tag	UNP P00491
C	-5	ASP	-	expression tag	UNP P00491
C	-4	LYS	-	expression tag	UNP P00491
C	-3	ASP	-	expression tag	UNP P00491
C	-2	PRO	-	expression tag	UNP P00491
C	-1	THR	-	expression tag	UNP P00491
C	0	LEU	-	expression tag	UNP P00491
C	16	TYR	TRP	engineered mutation	UNP P00491
C	51	SER	GLY	engineered mutation	UNP P00491
C	94	TYR	TRP	engineered mutation	UNP P00491
C	178	TYR	TRP	engineered mutation	UNP P00491
C	257	TRP	HIS	engineered mutation	UNP P00491
D	-34	MET	-	initiating methionine	UNP P00491
D	-33	ARG	-	expression tag	UNP P00491
D	-32	GLY	-	expression tag	UNP P00491
D	-31	SER	-	expression tag	UNP P00491
D	-30	HIS	-	expression tag	UNP P00491
D	-29	HIS	-	expression tag	UNP P00491
D	-28	HIS	-	expression tag	UNP P00491
D	-27	HIS	-	expression tag	UNP P00491
D	-26	HIS	-	expression tag	UNP P00491
D	-25	HIS	-	expression tag	UNP P00491
D	-24	GLY	-	expression tag	UNP P00491
D	-23	MET	-	expression tag	UNP P00491
D	-22	ALA	-	expression tag	UNP P00491
D	-21	SER	-	expression tag	UNP P00491
D	-20	MET	-	expression tag	UNP P00491
D	-19	THR	-	expression tag	UNP P00491
D	-18	GLY	-	expression tag	UNP P00491
D	-17	GLY	-	expression tag	UNP P00491
D	-16	GLN	-	expression tag	UNP P00491
D	-15	GLN	-	expression tag	UNP P00491
D	-14	MET	-	expression tag	UNP P00491
D	-13	GLY	-	expression tag	UNP P00491
D	-12	ARG	-	expression tag	UNP P00491

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-11	ASP	-	expression tag	UNP P00491
D	-10	LEU	-	expression tag	UNP P00491
D	-9	TYR	-	expression tag	UNP P00491
D	-8	ASP	-	expression tag	UNP P00491
D	-7	ASP	-	expression tag	UNP P00491
D	-6	ASP	-	expression tag	UNP P00491
D	-5	ASP	-	expression tag	UNP P00491
D	-4	LYS	-	expression tag	UNP P00491
D	-3	ASP	-	expression tag	UNP P00491
D	-2	PRO	-	expression tag	UNP P00491
D	-1	THR	-	expression tag	UNP P00491
D	0	LEU	-	expression tag	UNP P00491
D	16	TYR	TRP	engineered mutation	UNP P00491
D	51	SER	GLY	engineered mutation	UNP P00491
D	94	TYR	TRP	engineered mutation	UNP P00491
D	178	TYR	TRP	engineered mutation	UNP P00491
D	257	TRP	HIS	engineered mutation	UNP P00491
E	-34	MET	-	initiating methionine	UNP P00491
E	-33	ARG	-	expression tag	UNP P00491
E	-32	GLY	-	expression tag	UNP P00491
E	-31	SER	-	expression tag	UNP P00491
E	-30	HIS	-	expression tag	UNP P00491
E	-29	HIS	-	expression tag	UNP P00491
E	-28	HIS	-	expression tag	UNP P00491
E	-27	HIS	-	expression tag	UNP P00491
E	-26	HIS	-	expression tag	UNP P00491
E	-25	HIS	-	expression tag	UNP P00491
E	-24	GLY	-	expression tag	UNP P00491
E	-23	MET	-	expression tag	UNP P00491
E	-22	ALA	-	expression tag	UNP P00491
E	-21	SER	-	expression tag	UNP P00491
E	-20	MET	-	expression tag	UNP P00491
E	-19	THR	-	expression tag	UNP P00491
E	-18	GLY	-	expression tag	UNP P00491
E	-17	GLY	-	expression tag	UNP P00491
E	-16	GLN	-	expression tag	UNP P00491
E	-15	GLN	-	expression tag	UNP P00491
E	-14	MET	-	expression tag	UNP P00491
E	-13	GLY	-	expression tag	UNP P00491
E	-12	ARG	-	expression tag	UNP P00491
E	-11	ASP	-	expression tag	UNP P00491
E	-10	LEU	-	expression tag	UNP P00491

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-9	TYR	-	expression tag	UNP P00491
E	-8	ASP	-	expression tag	UNP P00491
E	-7	ASP	-	expression tag	UNP P00491
E	-6	ASP	-	expression tag	UNP P00491
E	-5	ASP	-	expression tag	UNP P00491
E	-4	LYS	-	expression tag	UNP P00491
E	-3	ASP	-	expression tag	UNP P00491
E	-2	PRO	-	expression tag	UNP P00491
E	-1	THR	-	expression tag	UNP P00491
E	0	LEU	-	expression tag	UNP P00491
E	16	TYR	TRP	engineered mutation	UNP P00491
E	51	SER	GLY	engineered mutation	UNP P00491
E	94	TYR	TRP	engineered mutation	UNP P00491
E	178	TYR	TRP	engineered mutation	UNP P00491
E	257	TRP	HIS	engineered mutation	UNP P00491
F	-34	MET	-	initiating methionine	UNP P00491
F	-33	ARG	-	expression tag	UNP P00491
F	-32	GLY	-	expression tag	UNP P00491
F	-31	SER	-	expression tag	UNP P00491
F	-30	HIS	-	expression tag	UNP P00491
F	-29	HIS	-	expression tag	UNP P00491
F	-28	HIS	-	expression tag	UNP P00491
F	-27	HIS	-	expression tag	UNP P00491
F	-26	HIS	-	expression tag	UNP P00491
F	-25	HIS	-	expression tag	UNP P00491
F	-24	GLY	-	expression tag	UNP P00491
F	-23	MET	-	expression tag	UNP P00491
F	-22	ALA	-	expression tag	UNP P00491
F	-21	SER	-	expression tag	UNP P00491
F	-20	MET	-	expression tag	UNP P00491
F	-19	THR	-	expression tag	UNP P00491
F	-18	GLY	-	expression tag	UNP P00491
F	-17	GLY	-	expression tag	UNP P00491
F	-16	GLN	-	expression tag	UNP P00491
F	-15	GLN	-	expression tag	UNP P00491
F	-14	MET	-	expression tag	UNP P00491
F	-13	GLY	-	expression tag	UNP P00491
F	-12	ARG	-	expression tag	UNP P00491
F	-11	ASP	-	expression tag	UNP P00491
F	-10	LEU	-	expression tag	UNP P00491
F	-9	TYR	-	expression tag	UNP P00491
F	-8	ASP	-	expression tag	UNP P00491

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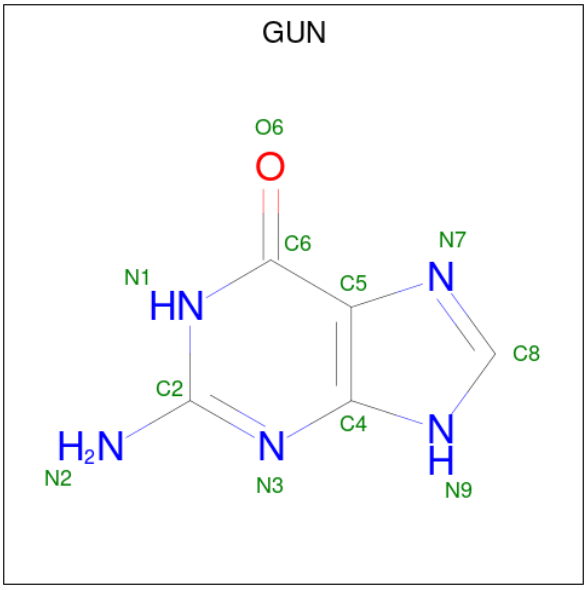
Chain	Residue	Modelled	Actual	Comment	Reference
F	-7	ASP	-	expression tag	UNP P00491
F	-6	ASP	-	expression tag	UNP P00491
F	-5	ASP	-	expression tag	UNP P00491
F	-4	LYS	-	expression tag	UNP P00491
F	-3	ASP	-	expression tag	UNP P00491
F	-2	PRO	-	expression tag	UNP P00491
F	-1	THR	-	expression tag	UNP P00491
F	0	LEU	-	expression tag	UNP P00491
F	16	TYR	TRP	engineered mutation	UNP P00491
F	51	SER	GLY	engineered mutation	UNP P00491
F	94	TYR	TRP	engineered mutation	UNP P00491
F	178	TYR	TRP	engineered mutation	UNP P00491
F	257	TRP	HIS	engineered mutation	UNP P00491

- Molecule 2 is GUANINE (three-letter code: GUN) (formula: $C_5H_5N_5O$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	11	5	5	1	0	0
2	B	1	11	5	5	1	0	0
2	C	1	11	5	5	1	0	0
2	D	1	11	5	5	1	0	0
2	E	1	11	5	5	1	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	F	1	11	5	5	1	0	0

- Molecule 3 is water.

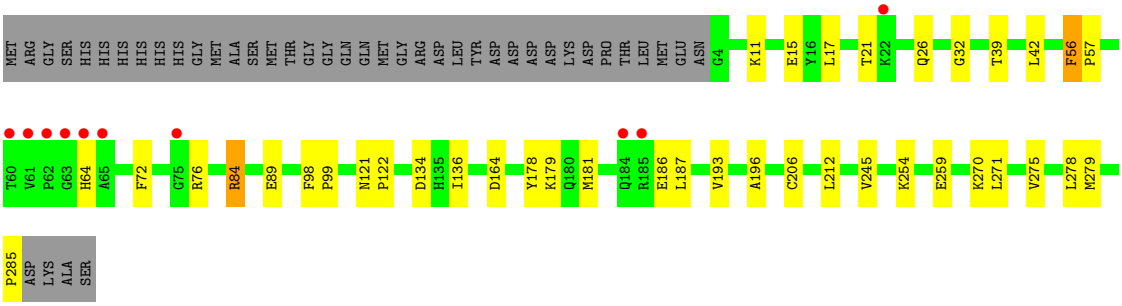
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	72	72	72	0	0
			Total	O		
3	B	80	80	80	0	0
			Total	O		
3	C	59	59	59	0	0
			Total	O		
3	D	40	40	40	0	0
			Total	O		
3	E	45	45	45	0	0
			Total	O		
3	F	9	9	9	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

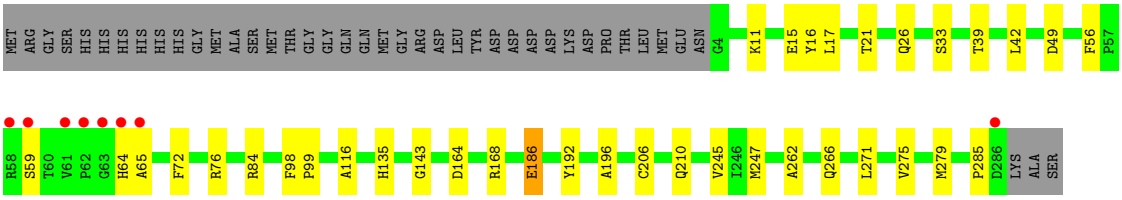
• Molecule 1: Purine nucleoside phosphorylase

Chain A:



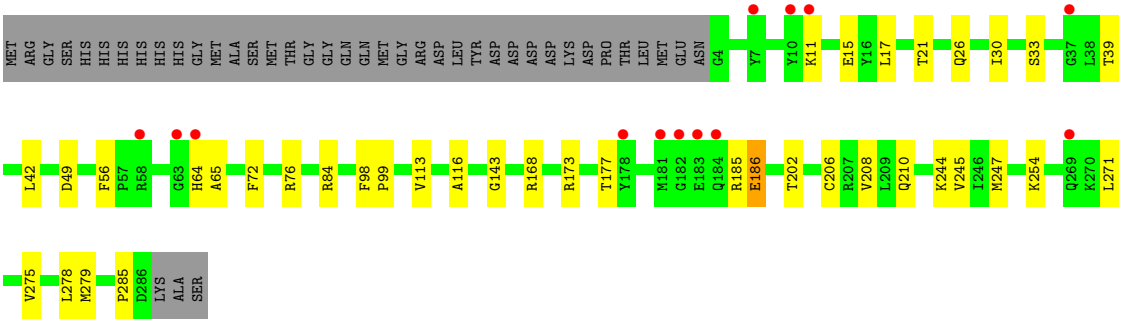
• Molecule 1: Purine nucleoside phosphorylase

Chain B:



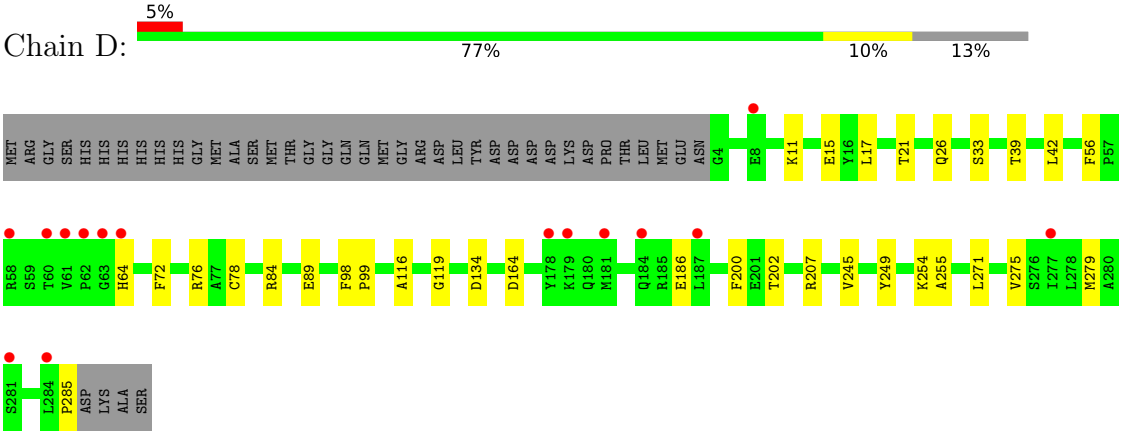
• Molecule 1: Purine nucleoside phosphorylase

Chain C:



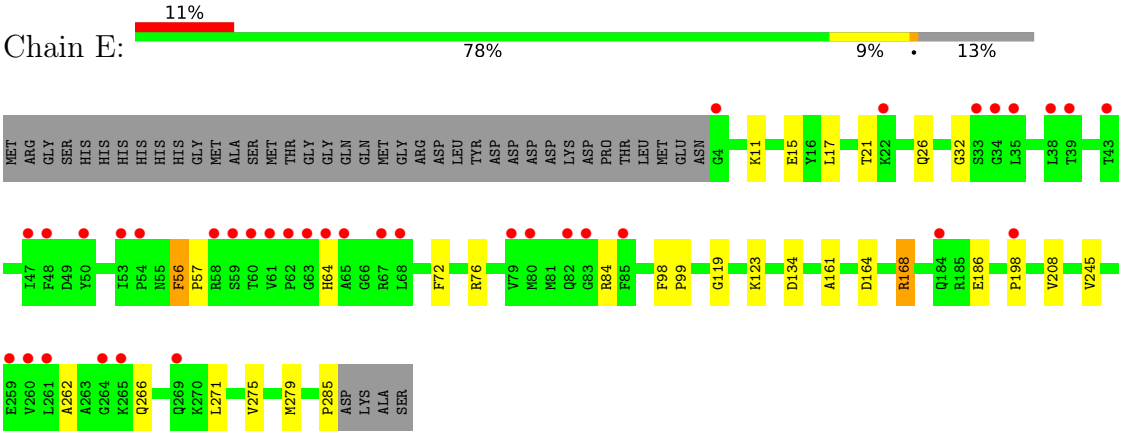
• Molecule 1: Purine nucleoside phosphorylase

Chain D:



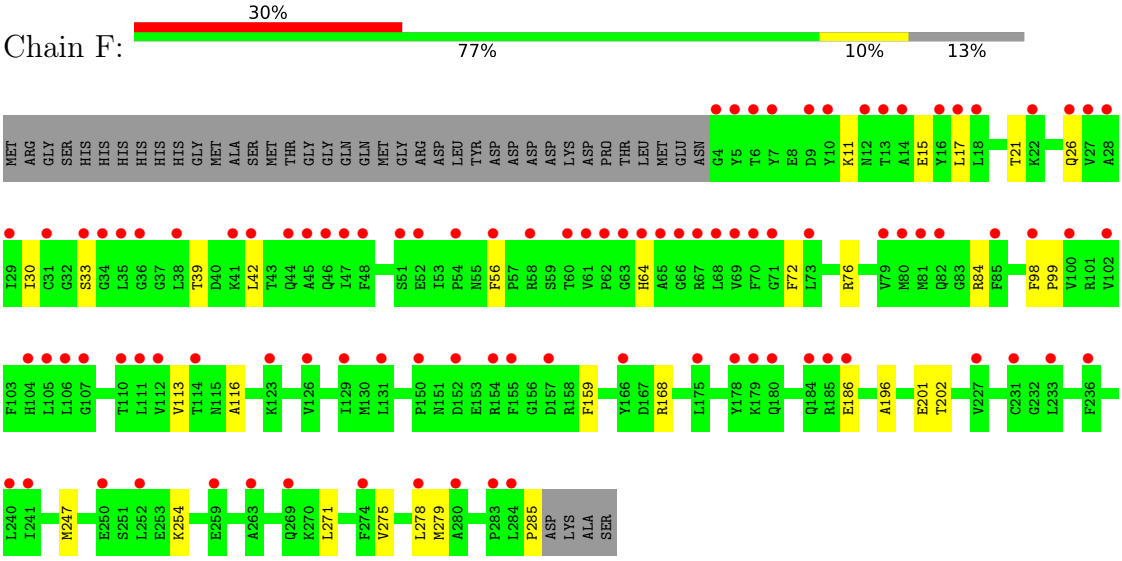
• Molecule 1: Purine nucleoside phosphorylase

Chain E:



• Molecule 1: Purine nucleoside phosphorylase

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	77.55Å 129.68Å 104.35Å 90.00° 105.29° 90.00°	Depositor
Resolution (Å)	49.04 – 2.60 49.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.04-2.60) 99.9 (49.00-2.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	2.13 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.222 , 0.261 0.220 , 0.260	Depositor DCC
R_{free} test set	3106 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	60.0	Xtriage
Anisotropy	0.290	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 50.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	13632	wwPDB-VP
Average B, all atoms (Å^2)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GUN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	0.63	0/2259	0.76	0/3056
1	B	0.67	0/2269	0.72	0/3069
1	C	0.55	0/2275	0.65	0/3077
1	D	0.55	0/2270	0.67	0/3070
1	E	0.50	0/2253	0.62	0/3048
1	F	0.43	0/2253	0.61	0/3048
All	All	0.56	0/13579	0.67	0/18368

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2206	0	2189	26	0
1	B	2216	0	2197	27	1
1	C	2219	0	2202	26	0
1	D	2214	0	2202	21	1
1	E	2203	0	2184	22	0
1	F	2203	0	2184	16	0
2	A	11	0	5	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	11	0	5	0	0
2	C	11	0	5	0	0
2	D	11	0	5	0	0
2	E	11	0	5	0	0
2	F	11	0	5	2	0
3	A	72	0	0	2	0
3	B	80	0	0	4	0
3	C	59	0	0	3	0
3	D	40	0	0	0	0
3	E	45	0	0	5	0
3	F	9	0	0	1	0
All	All	13632	0	13188	123	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (123) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:206[B]:CYS:SG	1:C:245:VAL:CG1	2.34	1.14
1:A:89:GLU:HG2	3:A:418:HOH:O	1.50	1.08
1:C:206[B]:CYS:SG	1:C:245:VAL:HG11	1.94	1.06
1:C:206[B]:CYS:SG	1:C:245:VAL:HG12	1.97	1.02
1:A:206[B]:CYS:SG	1:A:245:VAL:CG1	2.58	0.92
1:B:206:CYS:SG	1:B:245:VAL:CG1	2.61	0.89
1:F:201:GLU:OE2	2:F:301:GUN:N2	2.05	0.88
1:B:206:CYS:SG	1:B:245:VAL:HG11	2.17	0.85
1:A:259:GLU:HG3	3:A:459:HOH:O	1.77	0.84
1:A:206[B]:CYS:SG	1:A:245:VAL:HG11	2.19	0.83
1:A:206[B]:CYS:SG	1:A:245:VAL:HG12	2.18	0.83
1:B:49:ASP:HB3	3:B:475:HOH:O	1.83	0.79
1:E:198:PRO:O	1:F:159:PHE:HD1	1.68	0.77
1:B:206:CYS:SG	1:B:245:VAL:HG12	2.26	0.76
1:A:11:LYS:HE2	1:A:15:GLU:OE2	1.92	0.70
1:C:49:ASP:HB3	3:C:458:HOH:O	1.91	0.70
1:E:32:GLY:HA2	3:E:436:HOH:O	1.93	0.68
1:D:89:GLU:HG2	3:E:432:HOH:O	1.95	0.67
1:C:244:LYS:HE2	3:C:459:HOH:O	1.94	0.67
1:F:11:LYS:HE2	1:F:15:GLU:OE2	1.98	0.64
1:E:11:LYS:HE2	1:E:15:GLU:OE2	1.98	0.64
1:D:11:LYS:HE2	1:D:15:GLU:OE2	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:11:LYS:HE2	1:C:15:GLU:OE2	1.99	0.63
1:B:11:LYS:HE2	1:B:15:GLU:OE2	1.98	0.63
1:C:210:GLN:OE1	1:C:247[B]:MET:SD	2.57	0.63
1:F:201:GLU:CD	2:F:301:GUN:HN21	1.99	0.61
1:C:65:ALA:HB3	3:C:458:HOH:O	2.01	0.59
1:C:206[B]:CYS:HG	1:C:245:VAL:HG11	1.64	0.59
1:D:202:THR:HB	1:E:134:ASP:OD1	2.04	0.57
1:D:271:LEU:O	1:D:275:VAL:HG23	2.04	0.57
1:B:59:SER:HB2	3:B:449:HOH:O	2.03	0.57
1:D:164:ASP:OD2	1:F:254:LYS:NZ	2.33	0.56
1:C:271:LEU:O	1:C:275:VAL:HG23	2.07	0.55
1:D:254:LYS:NZ	1:E:164:ASP:OD2	2.36	0.55
1:D:254:LYS:HD2	1:E:164:ASP:OD2	2.08	0.54
1:F:271:LEU:O	1:F:275:VAL:HG23	2.08	0.53
1:B:98:PHE:HB3	1:B:99:PRO:HD3	1.88	0.53
1:E:168:ARG:HD3	3:E:411:HOH:O	2.09	0.53
1:A:76:ARG:HG2	1:A:279:MET:HE3	1.90	0.53
1:A:271:LEU:O	1:A:275:VAL:HG23	2.09	0.52
1:B:65:ALA:HB3	3:B:475:HOH:O	2.11	0.51
1:E:271:LEU:O	1:E:275:VAL:HG23	2.09	0.51
1:E:98:PHE:HB3	1:E:99:PRO:HD3	1.94	0.50
1:B:271:LEU:O	1:B:275:VAL:HG23	2.12	0.50
1:D:134:ASP:OD1	1:F:202:THR:HB	2.13	0.49
1:A:98:PHE:HB3	1:A:99:PRO:HD3	1.95	0.48
1:B:76:ARG:HG2	1:B:279:MET:HE3	1.94	0.48
1:B:206:CYS:HB3	1:B:247:MET:SD	2.53	0.48
1:D:72:PHE:HA	1:D:76:ARG:O	2.14	0.48
1:B:210:GLN:OE1	1:B:247:MET:SD	2.72	0.48
1:C:17:LEU:O	1:C:21:THR:HG22	2.13	0.48
1:C:76:ARG:HG2	1:C:279:MET:HE3	1.96	0.48
1:C:72:PHE:HA	1:C:76:ARG:O	2.14	0.48
1:D:42:LEU:HD21	1:D:78[B]:CYS:SG	2.54	0.48
1:C:98:PHE:HB3	1:C:99:PRO:HD3	1.96	0.47
1:F:196:ALA:O	3:F:408:HOH:O	2.20	0.47
1:B:76:ARG:HB3	1:B:279:MET:HE2	1.97	0.47
1:F:76:ARG:HG2	1:F:279:MET:HE3	1.97	0.47
1:F:17:LEU:O	1:F:21:THR:HG22	2.16	0.46
1:A:134:ASP:OD1	1:C:202:THR:HB	2.16	0.46
1:E:119:GLY:O	1:E:245:VAL:HG23	2.16	0.46
1:A:32:GLY:HA2	1:A:84:ARG:HH21	1.80	0.45
1:A:17:LEU:O	1:A:21:THR:HG22	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:GLN:HG3	1:B:285:PRO:HG3	1.98	0.45
1:A:212:LEU:HB3	1:C:208:VAL:HG22	1.99	0.45
1:D:249:TYR:O	1:E:168:ARG:NH2	2.49	0.45
1:A:196:ALA:CB	1:B:143:GLY:HA2	2.47	0.45
1:E:76:ARG:HG2	1:E:279:MET:HE3	1.99	0.45
1:A:164:ASP:OD2	1:C:254:LYS:NZ	2.41	0.45
1:E:17:LEU:O	1:E:21:THR:HG22	2.16	0.44
1:A:72:PHE:HA	1:A:76:ARG:O	2.17	0.44
1:D:76:ARG:HB3	1:D:279:MET:HE2	1.99	0.44
1:D:33:SER:HB2	1:D:116:ALA:HB2	1.99	0.44
1:D:119:GLY:O	1:D:245:VAL:HG23	2.17	0.44
1:F:72:PHE:HA	1:F:76:ARG:O	2.18	0.44
1:F:98:PHE:HB3	1:F:99:PRO:HD3	1.99	0.43
1:B:72:PHE:HA	1:B:76:ARG:O	2.18	0.43
1:C:185:ARG:HE	1:C:185:ARG:HB3	1.69	0.43
1:A:179:LYS:HD3	1:A:179:LYS:HA	1.86	0.43
1:C:186:GLU:H	1:C:186:GLU:HG3	1.68	0.43
1:E:123:LYS:NZ	3:E:422:HOH:O	2.51	0.43
1:B:17:LEU:O	1:B:21:THR:HG22	2.18	0.43
1:D:200:PHE:HB2	1:E:161:ALA:HA	2.01	0.43
1:E:72:PHE:HA	1:E:76:ARG:O	2.19	0.43
1:F:26:GLN:HG3	1:F:285:PRO:HG3	2.00	0.43
1:A:56:PHE:HA	1:A:57:PRO:HD3	1.92	0.42
1:D:17:LEU:O	1:D:21:THR:HG22	2.19	0.42
1:A:254:LYS:NZ	1:B:164:ASP:OD2	2.42	0.42
1:E:56:PHE:HA	1:E:57:PRO:HD3	1.95	0.42
1:B:59:SER:CB	3:B:449:HOH:O	2.64	0.42
1:E:26:GLN:HG3	1:E:285:PRO:HG3	2.00	0.42
1:A:121:ASN:HA	1:A:122:PRO:HD3	1.83	0.42
1:D:39:THR:O	1:D:42:LEU:HB2	2.19	0.42
1:A:136:ILE:HB	1:A:193:VAL:HG23	2.02	0.41
1:B:186:GLU:H	1:B:186:GLU:HG3	1.71	0.41
1:B:262:ALA:O	1:B:266:GLN:HG2	2.20	0.41
1:D:255:ALA:O	1:E:161:ALA:HB2	2.20	0.41
1:B:135:HIS:HA	1:B:192:TYR:O	2.20	0.41
1:B:76:ARG:HA	1:B:76:ARG:HD2	1.77	0.41
1:C:76:ARG:HA	1:C:76:ARG:HD2	1.81	0.41
1:B:39:THR:O	1:B:42:LEU:HB2	2.21	0.41
1:C:173:ARG:O	1:C:177:THR:HG23	2.21	0.41
1:D:26:GLN:HG3	1:D:285:PRO:HG3	2.02	0.41
1:E:208:VAL:HG23	3:E:433:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:GLN:HG3	1:A:285:PRO:HG3	2.03	0.41
1:A:76:ARG:HA	1:A:76:ARG:HD2	1.77	0.41
1:B:196:ALA:CB	1:C:143:GLY:HA2	2.51	0.41
1:C:26:GLN:HG3	1:C:285:PRO:HG3	2.01	0.41
1:C:33:SER:HB2	1:C:116:ALA:HB2	2.03	0.41
1:C:39:THR:O	1:C:42:LEU:HB2	2.21	0.41
1:F:33:SER:HB2	1:F:116:ALA:HB2	2.03	0.41
1:A:39:THR:O	1:A:42:LEU:HB2	2.22	0.40
1:A:178:TYR:CE1	1:A:187:LEU:HD13	2.56	0.40
1:E:262:ALA:O	1:E:266:GLN:HG2	2.21	0.40
1:A:181:MET:HE1	1:A:270:LYS:HG3	2.03	0.40
1:F:39:THR:O	1:F:42:LEU:HB2	2.21	0.40
1:B:16:TYR:CD2	1:B:16:TYR:C	2.94	0.40
1:B:33:SER:HB2	1:B:116:ALA:HB2	2.02	0.40
1:D:76:ARG:HA	1:D:76:ARG:HD2	1.81	0.40
1:E:76:ARG:HB3	1:E:279:MET:HE2	2.03	0.40
1:F:30:ILE:HD12	1:F:113:VAL:HG12	2.02	0.40
1:C:30:ILE:HD12	1:C:113:VAL:HG12	2.03	0.40
1:D:98:PHE:HB3	1:D:99:PRO:HD3	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:186:GLU:OE2	1:D:207[B]:ARG:NE[2_545]	2.05	0.15

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	281/324 (87%)	272 (97%)	9 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	282/324 (87%)	277 (98%)	5 (2%)	0	100	100
1	C	283/324 (87%)	277 (98%)	6 (2%)	0	100	100
1	D	282/324 (87%)	277 (98%)	5 (2%)	0	100	100
1	E	280/324 (86%)	275 (98%)	5 (2%)	0	100	100
1	F	280/324 (86%)	274 (98%)	6 (2%)	0	100	100
All	All	1688/1944 (87%)	1652 (98%)	36 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	235/269 (87%)	230 (98%)	5 (2%)	53	77
1	B	236/269 (88%)	231 (98%)	5 (2%)	53	77
1	C	237/269 (88%)	231 (98%)	6 (2%)	47	73
1	D	236/269 (88%)	232 (98%)	4 (2%)	60	81
1	E	234/269 (87%)	229 (98%)	5 (2%)	53	77
1	F	234/269 (87%)	227 (97%)	7 (3%)	41	67
All	All	1412/1614 (88%)	1380 (98%)	32 (2%)	50	75

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	PHE
1	A	64	HIS
1	A	84	ARG
1	A	186	GLU
1	A	278	LEU
1	B	56	PHE
1	B	64	HIS
1	B	84	ARG

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Mol	Chain	Res	Type
1	B	168	ARG
1	B	186	GLU
1	C	56	PHE
1	C	64	HIS
1	C	84	ARG
1	C	168	ARG
1	C	186	GLU
1	C	278	LEU
1	D	56	PHE
1	D	64	HIS
1	D	84	ARG
1	D	186	GLU
1	E	56	PHE
1	E	64	HIS
1	E	84	ARG
1	E	168	ARG
1	E	186	GLU
1	F	56	PHE
1	F	64	HIS
1	F	84	ARG
1	F	168	ARG
1	F	186	GLU
1	F	247	MET
1	F	278	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	188	GLN
1	B	243	ASN
1	C	243	ASN
1	D	243	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	GUN	A	301	-	7,12,12	1.06	0	8,17,17	1.79	3 (37%)
2	GUN	C	301	-	7,12,12	1.38	2 (28%)	8,17,17	1.81	3 (37%)
2	GUN	B	301	-	7,12,12	1.23	1 (14%)	8,17,17	2.14	4 (50%)
2	GUN	E	301	-	7,12,12	1.10	0	8,17,17	1.67	2 (25%)
2	GUN	D	301	-	7,12,12	1.34	1 (14%)	8,17,17	1.66	3 (37%)
2	GUN	F	301	-	7,12,12	1.08	0	8,17,17	1.55	2 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GUN	A	301	-	-	-	0/2/2/2
2	GUN	C	301	-	-	-	0/2/2/2
2	GUN	B	301	-	-	-	0/2/2/2
2	GUN	E	301	-	-	-	0/2/2/2
2	GUN	D	301	-	-	-	0/2/2/2
2	GUN	F	301	-	-	-	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	301	GUN	C6-N1	-2.51	1.34	1.37
2	C	301	GUN	C6-N1	-2.43	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	GUN	C2-N3	2.17	1.38	1.33
2	C	301	GUN	C2-N3	2.06	1.38	1.33

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	301	GUN	C8-N7-C5	3.86	110.34	102.99
2	C	301	GUN	C5-C6-N1	3.50	120.13	113.95
2	B	301	GUN	C2-N1-C6	-2.98	119.62	125.10
2	E	301	GUN	C8-N7-C5	2.93	108.57	102.99
2	B	301	GUN	C5-C6-N1	2.87	119.02	113.95
2	D	301	GUN	C8-N7-C5	2.84	108.40	102.99
2	A	301	GUN	O6-C6-C5	-2.72	119.05	124.37
2	F	301	GUN	C8-N7-C5	2.53	107.81	102.99
2	D	301	GUN	C5-C6-N1	2.41	118.20	113.95
2	A	301	GUN	C5-C6-N1	2.35	118.10	113.95
2	C	301	GUN	O6-C6-C5	-2.28	119.92	124.37
2	D	301	GUN	C2-N1-C6	-2.18	121.09	125.10
2	B	301	GUN	O6-C6-C5	-2.10	120.26	124.37
2	C	301	GUN	C2-N1-C6	-2.08	121.26	125.10
2	E	301	GUN	C5-C6-N1	2.07	117.60	113.95
2	A	301	GUN	C2-N1-C6	-2.06	121.31	125.10
2	F	301	GUN	C5-C6-N1	2.04	117.55	113.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	301	GUN	2	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	282/324 (87%)	0.29	10 (3%)	44	36	34, 57, 100, 169	0
1	B	283/324 (87%)	0.12	8 (2%)	53	46	31, 48, 86, 165	0
1	C	283/324 (87%)	0.32	13 (4%)	32	26	33, 62, 103, 144	0
1	D	282/324 (87%)	0.43	15 (5%)	26	20	39, 63, 107, 169	0
1	E	282/324 (87%)	0.88	36 (12%)	3	2	38, 75, 123, 200	0
1	F	282/324 (87%)	1.79	97 (34%)	0	0	52, 112, 157, 192	0
All	All	1694/1944 (87%)	0.64	179 (10%)	6	4	31, 66, 138, 200	0

All (179) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	64	HIS	12.6
1	D	62	PRO	8.7
1	B	62	PRO	8.5
1	E	63	GLY	8.2
1	F	155	PHE	7.7
1	E	62	PRO	7.7
1	F	63	GLY	7.5
1	B	64	HIS	7.3
1	F	38	LEU	7.0
1	A	63	GLY	6.6
1	F	18	LEU	6.5
1	F	68	LEU	6.5
1	E	65	ALA	6.3
1	F	62	PRO	6.2
1	F	48	PHE	6.0
1	A	64	HIS	6.0
1	F	7	TYR	5.9
1	F	280	ALA	5.9
1	F	65	ALA	5.8

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Mol	Chain	Res	Type	RSRZ
1	B	63	GLY	5.8
1	F	58	ARG	5.8
1	F	100	VAL	5.7
1	F	52	GLU	5.6
1	E	58	ARG	5.5
1	F	22	LYS	5.5
1	F	106	LEU	5.5
1	F	14	ALA	5.4
1	E	38	LEU	5.4
1	D	64	HIS	5.4
1	F	184	GLN	5.4
1	F	107	GLY	5.2
1	B	61	VAL	5.1
1	E	35	LEU	5.1
1	F	61	VAL	5.0
1	E	53	ILE	5.0
1	F	10	TYR	4.9
1	E	59	SER	4.8
1	B	65	ALA	4.7
1	F	126	VAL	4.7
1	F	80	MET	4.7
1	E	39	THR	4.7
1	F	69	VAL	4.7
1	F	29	ILE	4.7
1	E	60	THR	4.6
1	F	4	GLY	4.5
1	F	154	ARG	4.4
1	D	61	VAL	4.4
1	A	62	PRO	4.4
1	F	17	LEU	4.1
1	F	269	GLN	4.1
1	D	63	GLY	4.1
1	F	157	ASP	4.1
1	F	51	SER	4.0
1	F	13	THR	3.9
1	E	34	GLY	3.9
1	C	269	GLN	3.9
1	F	71	GLY	3.9
1	E	265	LYS	3.8
1	F	274	PHE	3.8
1	D	184	GLN	3.7
1	E	61	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
1	C	184	GLN	3.7
1	F	41	LYS	3.7
1	B	58	ARG	3.7
1	F	28	ALA	3.7
1	F	26	GLN	3.7
1	F	45	ALA	3.6
1	A	65	ALA	3.6
1	F	27	VAL	3.6
1	F	111	LEU	3.6
1	F	81	MET	3.6
1	D	284	LEU	3.5
1	F	35	LEU	3.5
1	E	4	GLY	3.5
1	A	60	THR	3.5
1	F	6	THR	3.5
1	E	47	ILE	3.4
1	D	58	ARG	3.3
1	F	179	LYS	3.3
1	F	36	GLY	3.3
1	F	175	LEU	3.3
1	A	61	VAL	3.3
1	E	67	ARG	3.3
1	F	110	THR	3.2
1	F	34	GLY	3.2
1	E	50	TYR	3.2
1	D	8	GLU	3.2
1	B	286	ASP	3.2
1	C	183	GLU	3.2
1	F	123	LYS	3.2
1	E	260	VAL	3.1
1	F	33	SER	3.1
1	F	98	PHE	3.1
1	F	240	LEU	3.1
1	E	22	LYS	3.1
1	E	184	GLN	3.1
1	F	67	ARG	3.1
1	E	261	LEU	3.0
1	F	54	PRO	3.0
1	E	43	THR	3.0
1	F	31	CYS	3.0
1	E	80	MET	3.0
1	E	54	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
1	F	16	TYR	2.9
1	F	112	VAL	2.9
1	E	82	GLN	2.9
1	F	5	TYR	2.9
1	F	284	LEU	2.9
1	C	181	MET	2.9
1	F	178	TYR	2.9
1	F	73	LEU	2.8
1	F	263	ALA	2.8
1	F	102	VAL	2.8
1	E	33	SER	2.8
1	F	252	LEU	2.8
1	C	178	TYR	2.8
1	F	152	ASP	2.7
1	F	47	ILE	2.7
1	B	59	SER	2.7
1	F	42	LEU	2.6
1	F	105	LEU	2.6
1	F	278	LEU	2.6
1	A	184	GLN	2.6
1	F	259	GLU	2.6
1	D	181	MET	2.6
1	F	79	VAL	2.6
1	F	180	GLN	2.6
1	F	56	PHE	2.6
1	E	79	VAL	2.6
1	F	227	VAL	2.5
1	E	264	GLY	2.5
1	F	236	PHE	2.5
1	D	179	LYS	2.5
1	F	241	ILE	2.5
1	A	185	ARG	2.5
1	F	44	GLN	2.5
1	F	231	CYS	2.5
1	F	82	GLN	2.5
1	E	68	LEU	2.4
1	C	11	LYS	2.4
1	F	12	ASN	2.4
1	F	185	ARG	2.4
1	E	83	GLY	2.4
1	C	7	TYR	2.4
1	F	46	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	F	64	HIS	2.4
1	E	85	PHE	2.4
1	F	150	PRO	2.3
1	F	283	PRO	2.3
1	F	60	THR	2.3
1	D	277	ILE	2.3
1	D	281	SER	2.3
1	E	48	PHE	2.3
1	D	178	TYR	2.3
1	F	9	ASP	2.3
1	F	104	HIS	2.3
1	D	60	THR	2.2
1	F	129	ILE	2.2
1	C	37	GLY	2.2
1	F	166	TYR	2.2
1	C	58	ARG	2.2
1	D	187	LEU	2.2
1	F	250	GLU	2.1
1	C	10	TYR	2.1
1	C	64	HIS	2.1
1	F	233	LEU	2.1
1	C	63	GLY	2.1
1	F	186	GLU	2.1
1	E	259	GLU	2.1
1	F	114	THR	2.1
1	F	70	PHE	2.1
1	F	85	PHE	2.1
1	F	131	LEU	2.0
1	A	22	LYS	2.0
1	E	269	GLN	2.0
1	A	75	GLY	2.0
1	C	182	GLY	2.0
1	F	66	GLY	2.0
1	E	198	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GUN	F	301	11/11	0.92	0.16	55,57,58,58	0
2	GUN	E	301	11/11	0.93	0.17	64,66,68,69	0
2	GUN	D	301	11/11	0.97	0.14	42,43,44,46	0
2	GUN	A	301	11/11	0.98	0.15	37,37,39,39	0
2	GUN	B	301	11/11	0.98	0.15	40,41,43,43	0
2	GUN	C	301	11/11	0.98	0.17	38,44,45,46	0

6.5 Other polymers (i)

There are no such residues in this entry.